

#2

OIPE

## RAW SEQUENCE LISTING

DATE: 12/18/2001

PATENT APPLICATION: US/10/008,789

TIME: 16:17:53

Input Set : A:\RTS-0333 Sequence Listing.txt

Output Set: N:\CRF3\12182001\J008789.raw

**ENTERED**

6 <110> APPLICANT: C. Frank Bennett  
7 Kenneth Dobie  
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR  
6 EXPRESSION  
11 <130> FILE REFERENCE: RTS-0333  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/008,789  
C--> 13 <141> CURRENT FILING DATE: 2001-11-08  
13 <160> NUMBER OF SEQ ID NOS: 89  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 20  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
21 <220> FEATURE:  
23 <223> OTHER INFORMATION: Antisense Oligonucleotide  
25 <400> SEQUENCE: 1  
26 tccgtcatcg ctccctcaggg 20  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 20  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
36 <223> OTHER INFORMATION: Antisense Oligonucleotide  
38 <400> SEQUENCE: 2  
39 atgcattctg cccccaagga 20  
42 <210> SEQ ID NO: 3  
43 <211> LENGTH: 1755  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Homo sapiens  
47 <220> FEATURE:  
49 <220> FEATURE:  
50 <221> NAME/KEY: CDS  
51 <222> LOCATION: (160)...(1590)  
53 <400> SEQUENCE: 3  
54 cgccccgggca ggtcccaaaa ttagggggga agaggaaaaa aaaaagccag aaaaagtttt 60  
56 cttttctgga gtcccaaacg aggtgcggga cggaagaggg ggtgaaggcc agaggctcgg 120  
58 ggcttcaaga ccgctgtctg gagtccccct ttccaggcc atg tcg ggg ccc acc 174  
59 Met Ser Gly Pro Thr  
60 1 5  
62 tgg ctg ccc ccg aag cag ccg gag ccc gcc aga gcc cct cag ggg agg 222  
63 Trp Leu Pro Pro Lys Gln Pro Glu Pro Ala Arg Ala Pro Gln Gly Arg  
64 10 15 20  
66 gcg atc ccc cgc ggc acc ccg ggg cca cca ccg gcc cac gga gca gca 270  
67 Ala Ile Pro Arg Gly Thr Pro Gly Pro Pro Pro Ala His Gly Ala Ala  
68 25 30 35  
70 ctc cag ccc cac ccc agg gtc aat ttt tgc ccc ctt oca tct gag cag 318  
71 Leu Gln Pro His Pro Arg Val Asn Phe Cys Pro Leu Pro Ser Glu Gln  
72 40 45 50  
74 tgt tac cag gcc cca ggg gga ccg gag gat cgg ggg ccg gcg tgg gtg 366

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75	Cys	Tyr	Gln	Ala	Pro	Gly	Gly	Pro	Glu	Asp	Arg	Gly	Pro	Ala	Trp	Val	
76		55					60					65					
78	ggg	tcc	cat	gga	gta	ctc	cag	cac	acg	cag	ggg	ctc	cct	gca	gac	agg	414
79	Gly	Ser	His	Gly	Val	Leu	Gln	His	Thr	Gln	Gly	Leu	Pro	Ala	Asp	Arg	
80	70					75					80					85	
82	ggg	ggc	ctt	cgc	cct	gga	agc	ctg	gac	gcc	gag	ata	gac	ttg	ctg	agc	462
83	Gly	Gly	Leu	Arg	Pro	Gly	Ser	Leu	Asp	Ala	Glu	Ile	Asp	Leu	Leu	Ser	
84					90					95					100		
86	acc	acg	ctg	gcc	aaa	ctg	aat	ggg	ggt	cgg	ggt	cat	gcg	tca	cgg	cga	510
87	Thr	Thr	Leu	Ala	Lys	Leu	Asn	Gly	Gly	Arg	Gly	His	Ala	Ser	Arg	Arg	
88				105					110				115				
90	cca	gac	cga	cag	gca	tat	gag	ccc	ccg	cca	cct	cct	gcc	tac	cgc	acg	558
91	Pro	Asp	Arg	Gln	Ala	Tyr	Glu	Pro	Pro	Pro	Pro	Pro	Ala	Tyr	Arg	Thr	
92		120						125					130				
94	ggc	tcc	ctg	aag	cca	aat	cca	gcc	tcg	ccg	ctc	cca	gcg	tct	ccc	tat	606
95	Gly	Ser	Leu	Lys	Pro	Asn	Pro	Ala	Ser	Pro	Leu	Pro	Ala	Ser	Pro	Tyr	
96		135				140					145						
98	ggg	ggc	ccc	act	cca	gcc	tct	tac	act	acc	gcc	agc	acc	ccg	gct	ggc	654
99	Gly	Gly	Pro	Thr	Pro	Ala	Ser	Tyr	Thr	Thr	Ala	Ser	Thr	Pro	Ala	Gly	
100	150					155					160				165		
102	cca	gcc	ttc	ccc	gtg	caa	gtg	aag	gtg	gca	cag	cca	gtg	agg	ggc	tgc	702
103	Pro	Ala	Phe	Pro	Val	Gln	Val	Lys	Val	Ala	Gln	Pro	Val	Arg	Gly	Cys	
104				170						175					180		
106	ggc	cca	ccc	agg	cgg	gga	gcc	tct	cag	gct	tct	ggg	ccc	ctc	ccg	ggc	750
107	Gly	Pro	Pro	Arg	Arg	Gly	Ala	Ser	Gln	Ala	Ser	Gly	Pro	Leu	Pro	Gly	
108				185					190					195			
110	ccc	cac	ttt	cct	ctc	cca	ggc	cga	ggt	gaa	gtc	tgg	ggg	cct	ggc	tat	798
111	Pro	His	Phe	Pro	Leu	Pro	Gly	Arg	Gly	Glu	Val	Trp	Gly	Pro	Gly	Tyr	
112		200					205						210				
114	agg	agc	cag	aga	gag	cca	ggg	cca	ggg	gcc	aaa	gag	gaa	gct	gct	ggg	846
115	Arg	Ser	Gln	Arg	Glu	Pro	Gly	Pro	Gly	Ala	Lys	Glu	Glu	Ala	Ala	Gly	
116		215					220					225					
118	gtc	tct	ggc	cct	gca	gga	aga	gga	aga	gga	ggc	gag	cac	ggg	ccc	cag	894
119	Val	Ser	Gly	Pro	Ala	Gly	Arg	Gly	Arg	Gly	Gly	Glu	His	Gly	Pro	Gln	
120	230					235					240				245		
122	gtg	ccc	ctg	agc	cag	cct	cca	gag	gat	gag	ctg	gat	agg	ctg	acg	aag	942
123	Val	Pro	Leu	Ser	Gln	Pro	Pro	Glu	Asp	Glu	Leu	Asp	Arg	Leu	Thr	Lys	
124				250						255				260			
126	aag	ctg	gtt	cac	gac	atg	aac	cac	ccg	ccc	agc	ggg	gag	tac	ttt	ggc	990
127	Lys	Leu	Val	His	Asp	Met	Asn	His	Pro	Pro	Ser	Gly	Glu	Tyr	Phe	Gly	
128				265					270					275			
130	cag	tgt	ggt	ggc	tgc	gga	gaa	gat	gtg	gtt	ggg	gat	ggg	gct	ggg	gtt	1038
131	Gln	Cys	Gly	Gly	Cys	Gly	Glu	Asp	Val	Val	Gly	Asp	Gly	Ala	Gly	Val	
132			280					285					290				
134	gtg	gcc	ctt	gat	cgc	gtc	ttt	cac	gtg	ggc	tgc	ttt	gta	tgt	tct	aca	1086
135	Val	Ala	Leu	Asp	Arg	Val	Phe	His	Val	Gly	Cys	Phe	Val	Cys	Ser	Thr	
136		295				300						305					
138	tgc	cgg	gcc	cag	ctt	cgc	ggc	cag	cat	ttc	tac	gcc	gtg	gag	agg	agg	1134
139	Cys	Arg	Ala	Gln	Leu	Arg	Gly	Gln	His	Phe	Tyr	Ala	Val	Glu	Arg	Arg	

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```

140 310          315          320          325
142 gca tat tgc gag ggc tgc tac gtg gcc acc ctg gag aaa tgt gcc acg 1182
143 Ala Tyr Cys Glu Gly Cys Tyr Val Ala Thr Leu Glu Lys Cys Ala Thr
144          330          335          340
146 tgc tcc cag ccc atc ctg gac cgg atc ctg cgg gct atg ggg aag gcc 1230
147 Cys Ser Gln Pro Ile Leu Asp Arg Ile Leu Arg Ala Met Gly Lys Ala
148          345          350          355
150 tac cac cct ggc tgc ttc acc tgc gtg gtg tgt cac cgc ggc ctc gac 1278
151 Tyr His Pro Gly Cys Phe Thr Cys Val Val Cys His Arg Gly Leu Asp
152          360          365          370
154 ggc atc ccc ttc aca gtg gat gct acg agc cag atc cac tgt att gag 1326
155 Gly Ile Pro Phe Thr Val Asp Ala Thr Ser Gln Ile His Cys Ile Glu
156          375          380          385
158 gac ttt cac agg aag ttt gcc cca aga tgc tca gtg tgc ggt ggg gcc 1374
159 Asp Phe His Arg Lys Phe Ala Pro Arg Cys Ser Val Cys Gly Gly Ala
160 390          395          400          405
162 ata atg cct gag cca ggt cag gag gag act gtg aga att gtt gct ctg 1422
163 Ile Met Pro Glu Pro Gly Gln Glu Glu Thr Val Arg Ile Val Ala Leu
164          410          415          420
166 gat cga agt ttt cac att ggc tgt tac aag tgc gag gag tgt ggg ctg 1470
167 Asp Arg Ser Phe His Ile Gly Cys Tyr Lys Cys Glu Glu Cys Gly Leu
168          425          430          435
170 ctg ctc tcc tct gag ggc gag tgt cag ggc tgc tac ccg ctg gat ggg 1518
171 Leu Leu Ser Ser Glu Gly Glu Cys Gln Gly Cys Tyr Pro Leu Asp Gly
172          440          445          450
174 cac atc ttg tgc aag gcc tgc agc gcc tgg cgc atc cag gag ctc tca 1566
175 His Ile Leu Cys Lys Ala Cys Ser Ala Trp Arg Ile Gln Glu Leu Ser
176          455          460          465
178 gcc acc gtc acc act gac tgc tga gtcttctctag aagtacctgc tgggttctca 1620
179 Ala Thr Val Thr Thr Asp Cys
180 470          475
182 gttccagttc ccattctttg attgatcact ctccctgaca tccacctgta tgactttgtc 1680
184 accaaatgct gtcttctctt tctccaatca agaaataata atccctogag tttacaaaaa 1740
186 aaaaaaaaaa aaaaaa 1755
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 20
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR Primer
198 <400> SEQUENCE: 4
199 gctgcggaga agatgtggtt 20
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 21
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
209 <223> OTHER INFORMATION: PCR Primer
211 <400> SEQUENCE: 5

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## RAW SEQUENCE LISTING

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Output Set: N:\CRF3\12182001\J008789.raw

```

212 gcccgcatg tagaacatac a                                21
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 23
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Probe
224 <400> SEQUENCE: 6
225 ttgatcgcggt ctttcacgtg ggc                                23
228 <210> SEQ ID NO: 7
229 <211> LENGTH: 19
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
237 <400> SEQUENCE: 7
238 gaaggtgaag gtcggagtc                                19
241 <210> SEQ ID NO: 8
242 <211> LENGTH: 20
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <223> OTHER INFORMATION: PCR Primer
250 <400> SEQUENCE: 8
251 gaagatggtg atgggatttc                                20
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 20
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: PCR Probe
263 <400> SEQUENCE: 9
264 caagcttccc gttctcagcc                                20
267 <210> SEQ ID NO: 10
268 <211> LENGTH: 7001
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <220> FEATURE:
274 <221> NAME/KEY: exon
275 <222> LOCATION: (486)...(740)
276 <223> OTHER INFORMATION: exon 1
W--> 278 <221> NAME/KEY: exon:intron junction
279 <222> LOCATION: (740)...(741)
280 <223> OTHER INFORMATION: exon 1:intron 1
282 <221> NAME/KEY: intron
283 <222> LOCATION: (741)...(994)
284 <223> OTHER INFORMATION: intron 1
W--> 286 <221> NAME/KEY: intron:exon junction
287 <222> LOCATION: (994)...(995)

```

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Input Set : A:\RTS-0333 Sequence Listing.txt

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```
288 <223> OTHER INFORMATION: intron 1:exon 2
290 <221> NAME/KEY: exon
291 <222> LOCATION: (995)...(1122)
292 <223> OTHER INFORMATION: exon 2
W--> 294 <221> NAME/KEY: exon:intron junction
295 <222> LOCATION: (1122)...(1123)
296 <223> OTHER INFORMATION: exon 2:intron 2
298 <221> NAME/KEY: intron
299 <222> LOCATION: (1123)...(1241)
300 <223> OTHER INFORMATION: intron 2
W--> 302 <221> NAME/KEY: intron:exon junction
303 <222> LOCATION: (1241)...(1242)
304 <223> OTHER INFORMATION: intron 2:exon 3
306 <221> NAME/KEY: exon
307 <222> LOCATION: (1242)...(1367)
308 <223> OTHER INFORMATION: exon 3
W--> 310 <221> NAME/KEY: exon:intron junction
311 <222> LOCATION: (1367)...(1368)
312 <223> OTHER INFORMATION: exon 3:intron 3
314 <221> NAME/KEY: intron
315 <222> LOCATION: (1368)...(1628)
316 <223> OTHER INFORMATION: intron 3
W--> 318 <221> NAME/KEY: intron:exon junction
319 <222> LOCATION: (1628)...(1629)
320 <223> OTHER INFORMATION: intron 3:exon 4
322 <221> NAME/KEY: exon
323 <222> LOCATION: (1629)...(2000)
324 <223> OTHER INFORMATION: exon 4
W--> 326 <221> NAME/KEY: exon:intron junction
327 <222> LOCATION: (2000)...(2001)
328 <223> OTHER INFORMATION: exon 4:intron 4
330 <221> NAME/KEY: intron
331 <222> LOCATION: (2001)...(3503)
332 <223> OTHER INFORMATION: intron 4
W--> 334 <221> NAME/KEY: intron:exon junction
335 <222> LOCATION: (3503)...(3504)
336 <223> OTHER INFORMATION: intron 4:exon 5
338 <221> NAME/KEY: exon
339 <222> LOCATION: (3504)...(3597)
340 <223> OTHER INFORMATION: exon 5
W--> 342 <221> NAME/KEY: exon:intron junction
343 <222> LOCATION: (3597)...(3598)
344 <223> OTHER INFORMATION: exon 5:intron 5
346 <221> NAME/KEY: intron
347 <222> LOCATION: (3598)...(3707)
348 <223> OTHER INFORMATION: intron 5
W--> 350 <221> NAME/KEY: intron:exon junction
351 <222> LOCATION: (3707)...(3708)
352 <223> OTHER INFORMATION: intron 5:exon 6
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/008,789

DATE: 12/18/2001

TIME: 16:17:54

Input Set : A:\RTS-0333 Sequence Listing.txt

Output Set: N:\CRF3\12182001\J008789.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:286 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:294 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:302 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:310 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:334 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:342 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:350 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:366 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:374 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:382 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:398 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11